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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
09/620,680	07/20/00	VIDAL M	10974-239004

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EXAMINER	
SCHWARTZMAN, R	
ART UNIT	**PAPER NUMBER**
1636	9

DATE MAILED: 09/27/01

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

Office Action Summary	Application No. 09/620,680	Applicant(s) VIDAL ET AL.	
	Examiner Robert Schwartzman	Art Unit 1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136 (a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *20 July 2000 and 27 November 2000* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1 and 108-210* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1 and 108-210* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claims _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are objected to by the Examiner.

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. § 119

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgement is made of a claim for domestic priority under 35 U.S.C. § 119(e).

KATRINA TURNER
PATENT ANALYST

Attachment(s)

15)☐ Notice of References Cited (PTO-892)
16)☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
17)☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) 6 .
18)☐ Interview Summary (PTO-413) Paper No(s). _____ .
19)☐ Notice of Informal Patent Application (PTO-152)
20)☒ Other: *Notice To Comply With Requirements* .

DETAILED ACTION

This Office action is in response to the preliminary amendments filed July 20, 2000 (Paper No. 4) and November 27, 2000 (Paper No. 5). Claims 2-107 have been canceled and new claims 108-210 have been added. Claims 1 and 108-210 are pending in this application.

Specification

The specification contains nucleic acid and amino acid sequences (Figures 2, 10A, 21) that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures. Applicant must provide a paper copy and a computer readable copy of the Sequence Listing and a statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d). A full response to this Office Action must include a complete response to the requirement for a Sequence Listing.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 116, 141, 145 and 146 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 116 is vague and indefinite as it is drawn to a method in which the cell comprises two reporter genes linked to two different DNA binding protein recognition sites. However, the cell only contains one DNA binding moiety. It is therefore unclear how the one DNA binding moiety will specifically bind to two different DNA binding protein recognition sites.

Claim 141 is vague and indefinite as the word "DNA" is missing in step (a)(i) before "binding protein". Additionally, the term "physiologically relevant levels" is indefinite as it is not clear if it refers to the physiologically relevant level of the hybrid proteins in yeast or in the native cells in which the components of the hybrid protein are naturally found. Furthermore, since the hybrid protein is not a naturally occurring protein it cannot have a physiologically relevant level.

Additionally, the term "physiologically relevant' itself is indefinite as it is not clear to what it should be relevant, *i.e.*, what the "normal" level of protein expression.

Claim 145 is vague and indefinite as it refers to a first test RNA molecule but there is no second test RNA molecule.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless --
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.
>
> (e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

Claims 108, 109, 111, 112, 114, 115, 117, 119, 121-126, 128 and 131-136 are rejected under 35 U.S.C. 102(e) as being anticipated by Brent *et al.* (5,580,736).

Brent *et al.* teaches a method for determining whether a first test protein interacts with a second test protein involving providing a host cell comprising a reporter gene linked to a protein binding site, a first fusion gene expressing a first fusion protein comprising the first test protein linked to a protein which binds to the protein binding site and a second fusion gene expressing a second fusion protein comprising the second test protein linked to a gene activating moiety and measuring expression of the reporter gene as a measure of interaction between the two test proteins (column 2, lines 48-63). The host cell contains two different reporter genes and can be selectable genes (LEU2, HIS3, lacZ), or selectable/counterselectable genes (URA3, LYS2, GAL1) (column 7, line 33-column 8, line 28). Each reporter gene is under the control of a promoter containing an upstream binding site (such as the LexA operator). The fusion protein genes are introduced into the host cell as plasmids whereas the reporter gene can be on a plasmid and/or integrated into the host cell genome (column 10, lines 26-38). The gene encoding the second fusion protein is preferably isolated (column 2, lines 61-63).

Claim 141 is rejected under 35 U.S.C. 102(b) as being anticipated by Bartel *et al.* (In: Cell Interact. Dev. (1993) pp. 153-179.).

Bartel *et al.* teaches (entire document) the yeast two hybrid system in which a cell is provided which comprises two different reporter genes each operably linked to different promoters having identical DNA binding protein recognition sites, a first fusion gene encoding a

first hybrid protein comprising a test protein linked to a DNA binding moiety which binds to the DNA binding protein recognition site and a second fusion gene encoding a second hybrid protein comprising a test protein linked to a gene activating moiety and detection of reporter gene expression indicates that the first test protein interacts with the second test protein. Bartel *et al.* specifically states that it is advantageous to use two reporter genes linked to different promoters to reduce the number of false positives identified in the assay (page 176, first full paragraph).

Claims 142-144 are rejected under 35 U.S.C. 102(a) as being anticipated by Mendelsohn *et al.* (Curr. Opin. Biotechnol. (1994) 5:482).

Mendelsohn *et al.* teaches (entire document) the two hybrid assay and discusses various applications for this method. One application is the identification of compounds which modulate the binding between a first test protein and a second test protein (page 485, column 1, paragraph 2). Counterselection genes such as URA3, LYS2 and CYH2 can be used to select against transcription activation to facilitate the discovery of binding inhibitors. The second fusion gene comprising the gene activation moiety can be derived from a cDNA library (page 484).

Claims 108, 119, 121-127, 131, 138, 139 and 142-144 are rejected under 35 U.S.C. 102(a) as being anticipated by Le Douarin *et al.* (Nucleic Acids Res. (1995) 23:876).

Le Douarin *et al.* teaches (entire document) a modified version of the yeast two hybrid claim in which the target protein is expressed as a fusion with the DNA binding domain of the human estrogen receptor and the host cell contains an integrated URA3 reporter gene driven by one or three estrogen receptor response elements. This strain can be used by itself by introducing a plasmid encoding a protein linked to an activation domain such as VP16 or can be used in a mating assay by mating with a cell containing the HIS3 and lacZ reporter genes under the control of LexA binding sites. The presence of URA3 allows negative selection using 5-FOA, which is useful for screening activation domain fused libraries and for isolating compounds that inhibit protein-protein interactions.

Claims 149-210 are rejected under 35 U.S.C. 102(e) as being anticipated by Young *et al.* (U.S. Patent No. 5,989,808).

Young et al. teaches and claims two hybrid assay methods identical or nearly identical to the present claims. Thus, the present claims are anticipated.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(f) or (g) prior art under 35 U.S.C. 103(a).

Claims 131-136 are rejected under 35 U.S.C. 103(a) as being unpatentable over Bendixen *et al.* (Nucleic Acids Res. (1994) 22:1778) in view of Brent *et al.* (5,695,941).

Bendixen *et al.* teaches (entire document) a modified version of the yeast two hybrid system in which the construct encoding the first fusion protein is introduced into a mating

competent cell and the construct encoding the second fusion protein is introduced into the complementary mating competent cell. The two fusion proteins are brought together by mating the cells. Each mating competent cell further contains two reporter genes (either lacZ and LEU2 or lacZ and HIS3) each under the control of the GAL1 promoter containing GAL4 DNA binding domains and integrated into the genome of the host cell. The detection of interacting proteins was done with a protein of interest fused to the GAL4 DNA binding domain in one mating type and a cDNA library fused to the GAL4 activation domain in the other mating type. Interacting pairs were identified by detecting the expression of both reporter genes. Mated cells expressing the reporter genes were isolated and the plasmid encoding the fusion protein was isolated and sequenced. Bendixen *et al.* does not teach a reporter gene which is a counterselectable gene or a selectable/counterselectable gene or the location of the reporter gene on a plasmid. Brent *et al.* teaches that the reporter genes for the assay can be selectable genes (LEU2, HIS3, TRP1, lacZ), or selectable/counterselectable genes (URA3, LYS2, GAL1) (column 5, line 53-column 6, line 28). The reporter genes are introduced as plasmids (column 8, lines 16-27). It would have been *prima facie* obvious to one of ordinary skill in the art at the time the invention was made to use selectable or selectable/counterselectable reporter genes in the method of Bendixen *et al.* and to introduce the reporter genes into the host cell as a plasmid, motivated by the teachings of Brent *et al.* that all detectable reporter genes are equivalent and useful in the assay and that introduction of reporter genes on plasmids works as well as integrated reporter genes in the assay.

Claims 131-136 are rejected under 35 U.S.C. 103(a) as being unpatentable over Harper *et al.* (Cell (1993) 75:805) in view of Brent *et al.* (5,695,941).

Harper *et al.* teaches (page 806, column 2) a modified version of the yeast two hybrid system in which a mating competent cell comprising two integrated reporter genes (HIS3 and lacZ) and a chimeric gene encoding a test protein linked to an activation domain (such as GAL4) is mated to the complementary mating competent cell comprising a chimeric gene encoding a second test protein linked to a DNA binding domain (such as GAL4) and a lacZ reporter gene. The reporter genes are each under the control of the GAL1 promoter containing GAL4 DNA binding domains and integrated into the genome of the host cell. Interacting pairs were identified by detecting the expression of both reporter genes. Mated cells expressing the reporter genes were isolated and the plasmid encoding the fusion protein was isolated and sequenced. The protein linked to the activation domain is derived from a cDNA library. Harper *et al.* does not teach a reporter gene which is a counterselectable gene or a selectable/counterselectable gene or the location of the reporter gene on a plasmid. Brent *et al.* teaches that the reporter genes for the assay can be selectable genes (LEU2, HIS3, TRP1, lacZ), or selectable/counterselectable genes (URA3, LYS2, GAL1) (column 5, line 53-column 6, line 28). The reporter genes are introduced as plasmids (column 8, lines 16-27). It would have been *prima facie* obvious to one of ordinary skill in the art at the time the invention was made to use selectable or selectable/counterselectable reporter genes in the method of Harper *et al.* and to introduce the

reporter genes into the host cell as a plasmid, motivated by the teachings of Brent *et al.* that all detectable reporter genes are equivalent and useful in the assay and that introduction of reporter genes on plasmids works as well as integrated reporter genes in the assay.

Claim 137 is rejected under 35 U.S.C. 103(a) as being unpatentable over Brent *et al.* (5,695,941) in view of Bartel *et al.* (In: Cell Interact. Dev. (1993) pp. 153-179.).

Brent *et al.* teaches (column 2, lines 3-19) a modified version of the yeast two hybrid system in which the construct encoding the first fusion protein is introduced into a mating competent cell and the construct encoding the second fusion protein is introduced into the complementary mating competent cell. The two fusion proteins are brought together by mating the cells. Each cell further contains two different reporter genes and can be selectable genes (LEU2, HIS3, TRP1, lacZ), or selectable/counterselectable genes (URA3, LYS2, GAL1) (column 5, line 53-column 6, line 28). Each reporter gene is under the control of a promoter containing LexA binding sites. The fusion protein comprising the activation domain can be derived from a cDNA library (column 6, lines 40-51). The reporter genes and fusion protein genes are introduced as plasmids (column 8, lines 16-27). The DNA binding domain is derived from LexA (column 5, lines 9-31). Brent *et al.* does not teach two reporter genes linked to different promoters, integration of the reporter gene into the genome of the mating competent cell or gene activating moieties derived from GAL4, VP16 or Ace1. Bartel *et al.* teaches the

advantage of using two reporter genes linked to different promoters to reduce the number of false positives detected in the method (page 176, first full paragraph). Bartel *et al.* further teaches several host strains used for the two hybrid assays which contain the reporter genes integrated into the host cell genome (Table 2, page 161). Bartel *et al.* also teaches the use of the GAL4 or VP16 activation domains (Table 2, page 160). It would have been *prima facie* obvious to one of ordinary skill in the art at the time the invention was made to use two different promoters for the two reporter genes, motivated by the teaching of Bartel *et al.* that it results in a reduction in the number of false positives. One would further be motivated to use host cells comprising integrated reporter genes, as taught by Bartel *et al.*, based on the efficiency of not having to transform the host cells with an additional vector comprising the reporter genes along with the vectors comprising the fusion genes. Finally, one would be motivated to use several different activation domains, including GAL4 and VP16, based on the teachings of Bartel *et al.* that the method appears to work with any DNA binding and activation domains (page 158, first paragraph) and that the GAL4 and VP16 activation domains are available and commonly used.

Claims 129 and 130 are rejected under 35 U.S.C. 103(a) as being unpatentable over Brent *et al.* (5,580,736).

Brent *et al.* is applied as above. Brent *et al.* does not teach amplification or sequencing of the fusion gene from the isolated cell. It would have been *prima facie* obvious to one of ordinary

skill in the art at the time the invention was made to use the method of Brent *et al.* to identify proteins encoded by a cDNA library which interact with a protein of interest and to identify the protein by isolating the mated cell which expresses the reporter gene(s) and further isolating the fusion gene so that the cDNA portion can be sequenced. The isolation and sequencing of the fusion gene would involve standard recombinant DNA techniques well known to one of ordinary skill, including amplification of the fusion gene. The motivation to do this is implicit in the method, which is aimed at identifying unknown protein binding partners.

Claims 118 and 137 are rejected under 35 U.S.C. 103(a) as being unpatentable over Brent *et al.* (5,580,736) in view of Bartel *et al.* (In: Cell Interact. Dev. (1993) pp. 153-179.).

Brent *et al.* is applied as above. Brent *et al.* does not teach two reporter genes linked to different promoters. Bartel *et al.* teaches the advantage of using two reporter genes linked to different promoters to reduce the number of false positives detected in the method (page 176, first full paragraph). It would have been *prima facie* obvious to one of ordinary skill in the art at the time the invention was made to use two different promoters for the two reporter genes, motivated by the teaching of Bartel et all that it results in a reduction in the number of false positives.

Claims 128-130 are rejected under 35 U.S.C. 103(a) as being unpatentable over Le Douarin *et al.* (Nucleic Acids Res. (1995) 23:876).

Le Douarin *et al.* is applied as above. Le Douarin *et al.* does not teach isolation of the mated cell which expresses the reporter gene, isolation of the plasmid from the isolated cell or amplification, probing or sequencing of the fusion gene from the isolated cell. It would have been *prima facie* obvious to one of ordinary skill in the art at the time the invention was made to use the method of Brent *et al.* to identify proteins encoded by a cDNA library which interact with a protein of interest and to identify the protein by isolating the mated cell which expresses the reporter gene(s) and further isolating the fusion gene so that the cDNA portion can be sequenced. The isolation and sequencing of the fusion gene would involve standard recombinant DNA techniques well known to one of ordinary skill, including DNA amplification and hybridization probing of the fusion gene. The motivation to do this is implicit in the method, which is aimed at identifying unknown protein binding partners.

Claims 145-148 are rejected under 35 U.S.C. 103(a) as being unpatentable over Wickens (U.S. Patent No. 5,610015) *et al.* in view of Brent *et al.* (5,580,736).

Wickens *et al.* teaches (column 2, line 63-column 3, line 37) a method for determining whether a test RNA interacts with a test protein. This method involves providing a cell comprising a reporter gene linked to a DNA binding protein recognition site, a first chimeric gene encoding a first hybrid protein comprising a first RNA binding protein linked to a DNA binding protein which recognizes the site linked to the reporter gene, a second chimeric gene encoding a

second hybrid protein comprising a transcription activation domain linked to the test RNA binding protein and a third chimeric gene encoding a hybrid RNA comprising a first RNA sequence which binds to the first RNA binding protein and a second RNA sequence to be tested for interaction with the test RNA binding protein. Detection of reporter gene expression indicates that the test RNA interacts with the test protein. The reporter gene can be lacZ or other genes that allow direct selection (column 6, line 65-column 7, line 1). Wickens also teaches a method for determining whether a first RNA can interact with a second RNA (column 4, lines 22-37). This method comprises the first two chimeric genes discussed above, a third chimeric gene encoding a first hybrid RNA comprising a first RNA which binds to the first RNA binding protein and a second RNA sequence and a fourth chimeric gene encoding a second hybrid RNA comprising an RNA which binds to a second RNA binding protein and second RNA sequence. Interaction of the first RNA sequence and the second RNA sequence results in expression of the reporter gene. Wickens further teaches that the assays can be used to identify compounds which modulate the interaction between the test RNA and the test protein (column 4, lines 16-21). Wickens *et al.* does not teach a reporter gene which is a counterselectable or a selectable/counterselectable gene. Brent *et al.* teaches the two hybrid assay for detecting interactions between two proteins. Brent *et al.* teaches that selectable/counterselectable genes such as URA3, LYS2 and GAL1 can be used in the assay. It would have been *prima facie* obvious to one of ordinary skill in the art at the time the invention was made to use a reporter gene such as URA3, LYS2 or GAL1 in the RNA-protein or RNA-RNA interaction assays of Wickens *et al.*, motivated by the teaching of Wickens

et al. that any reporter gene that allows direct selection can be used and the teaching of Brent *et al.* that all reporter genes are equivalent and usable in these assay systems and the specific mention of URA3, LYS2 and GAL1.

Double Patenting

A rejection based on double patenting of the "same invention" type finds its support in the language of 35 U.S.C. 101 which states that "whoever invents or discovers any new and useful process ... may obtain a patent therefor ..." (Emphasis added). Thus, the term "same invention," in this context, means an invention drawn to identical subject matter. See *Miller v. Eagle Mfg. Co.*, 151 U.S. 186 (1894); *In re Ockert*, 245 F.2d 467, 114 USPQ 330 (CCPA 1957); and *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970).

A statutory type (35 U.S.C. 101) double patenting rejection can be overcome by canceling or amending the conflicting claims so they are no longer coextensive in scope. The filing of a terminal disclaimer cannot overcome a double patenting rejection based upon 35 U.S.C. 101.

Claim 1 is rejected under 35 U.S.C. 101 as claiming the same invention as that of claim 1 of prior U.S. Patent No. 5,965,368. This is a double patenting rejection.

The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. See *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed.

Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970);and, *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent is shown to be commonly owned with this application. See 37 CFR 1.130(b).

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

Claim 140 is rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claim 110 of U.S. Patent No. 5,955,280. Although the conflicting claims are not identical, they are not patentably distinct from each other because the issued claim, drawn to a cell comprising a fusion gene which expresses a hybrid protein comprising a test protein covalently bonded to a DNA binding moiety and a C-terminal tag, must use the genetic construct of the present claim.

Claims 142 and 143 are rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 18 and 26 of U.S. Patent No. 5,965,368. Although the conflicting claims are not identical, they are not patentably distinct from each other because the issued claims, drawn to determining whether a test compound disrupts binding between two proteins, anticipates the present claims drawn to determining whether a test compound affects binding between two test proteins.

Conclusion

Claims 1, 108, 109, 111, 112, 114-119 and 121-210 are rejected. Claims 110, 113 and 120 are objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims. Claims 1, 110, 113, 116, 120 and 140 are free of the prior art.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Robert Schwartzman whose telephone number is (703) 308-7307. The examiner can normally be reached on Monday through Friday from 6:30 AM to 4:00 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, George Elliott, can be reached at (703) 308-4003. The fax number for this group is (703) 305-3014.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703)-308-0196.

ROBERT A. SCHWARTZMAN
PRIMARY EXAMINER

September 25, 2001

Application No. 09/620,680

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

[X] 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

[X] 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

[X] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).

[ ] 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."

[ ] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

[ ] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

[ ] 7.

Other: _____

Applicant must provide:

[X] An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"

[X] An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

[X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.